

Supplemental Data for Zandvakili et al.

Sequences used in the GD-lacZ and *RhoAAA-lacZ* reporter assays. Sequences in FASTA format for all the constructs generated and tested in the transgenic reporter assays. Note, the *RhoAAA-lacZ* transgenic reporters contain three concatemers of each listed *RhoA* sequence.

>DCRE_WT

GGAATTTATGTCCGACAATATTTGGGAAATTAAATCATTCCCGCGGACAGTTTTATAGTGC GG GCGTGGC

>DCRE_AF

GGAATTTATGTCCGACAATATTTGGGTGATTGACATTTTTATTATGC GG GCGTGGC

>DCRE_AR

GGAATTTATGTCCGACAATATTTGGGTAATAAAAATGTCAATCATGC GG GCGTGGC

>DCRE_AR_HoxM

GGAATTTATGTCCGACAATATTTGGGTAAGCAAAATGTCAATCATGC GG GCGTGGC

>DCRE_HF

GGAATTTATGTCCGACAATATTTGGGCTATAAACTGTCCGCGGAATGATTTAATTTGC GG GCGTGGC

>DCRE+5

GGAATTTATGTCCGACAATATTTGGTGACCGAAATTAAATCATTCCCGCGGACAGTTTTATAGTGC GG GCGTGGC

>DCRE+10

GGAATTTATGTCCGACAATATTTGGCCGGTACGAAGAAATTAAATCATTCCCGCGGACAGTTTTATAGTGC GG GCGTGGC

>DCRE+15

GGAATTTATGTCCGACAATATTTGGATGAGAAGCCGTGCCGAAATTAAATCATTCCCGCGGACAGTTTTATAGTGC GG GCGTGGC

>DCRE+20

GGAATTTATGTCCGACAATATTTGGTGCCTATGAGAAGCCGTGCCGAAATTAAATCATTCCCGCGGACAGTTTTATAGTGC GG GCGTGGC

>DCRE_SlpM

GGAATTTATGTCCGACAATCGTTGGGAAATTAAATCATTCCCGCGGACAGTTTTATAGTGC GG GCGTGGC

>DCRE_Bap

GGAATTTATGTCCTGTTTATAAACAGAAATTAAATCATTCCCGCGGACAGTTTTATAGTGCGGGCGTGCC

>DCRE_Eve

GGAATTTATGTCCAAACAAACAAACGAAATTAAATCATTCCCGCGGACAGTTTTATAGTGCGGGCGTGCC

>DCRE_EveRC

GGAATTTATGTCTGTTTGTGTTGTTGAAATTAAATCATTCCCGCGGACAGTTTTATAGTGCGGGCGTGCC

>DCRE_BapC

GGAATTTATGTCCACAAATATTTGTGAAATTAAATCATTCCCGCGGACAGTTTTATAGTGCGGGCGTGCC

>RhoA_DF

TCGTTGCAGTTCATAAATTAAATCATTCCCGCGGACAGTTTTATAGTGCATATTCGCTGGT

>RhoA_DR

TCGTTGCAGTTCATCTATAAACTGTCCGCGGGAATGATTTAATTTTGCATATTCGCTGGT

>RhoA+5

TCGTTGCAGTTCAGGTCATTGATTGACATTTTTATTATGCATATTCGCTGGT

>RhoA+10

TCGTTGCAGTTCAGCTCGGGTCATTGATTGACATTTTTATTATGCATATTCGCTGGT

Supplemental Figures:

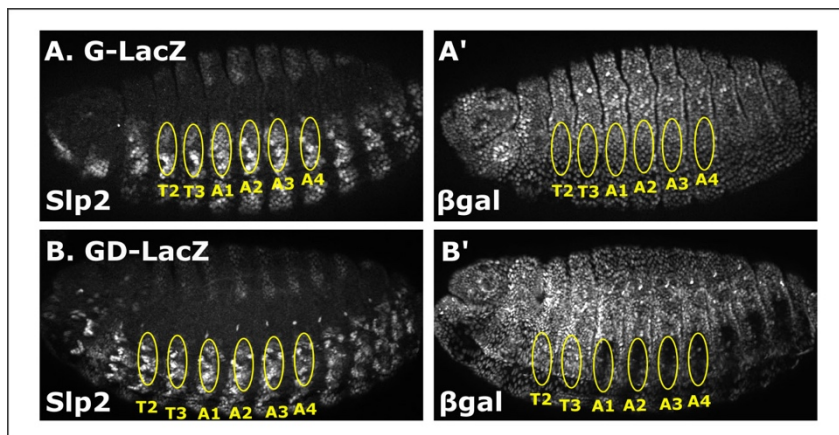


Figure S1. Quantification strategy of β -gal intensity in 3xGBE-DCRE-LacZ reporter assays.

Lateral views of Stage 15 *Drosophila* embryos stained for Slp2 and β -gal. **(A-B)** Slp2-positive

cells in the lateral ectoderm of the T2-A4 segments were manually encircled to define regions-of-interest (ROIs). **(A'-B')** The ROIs were used to measure β -gal intensity in a separate channel. As explained in the Material and Methods, the mean β -gal intensity measurements were determined by subtracting from background and normalizing to β -gal intensity of the T3 segment.

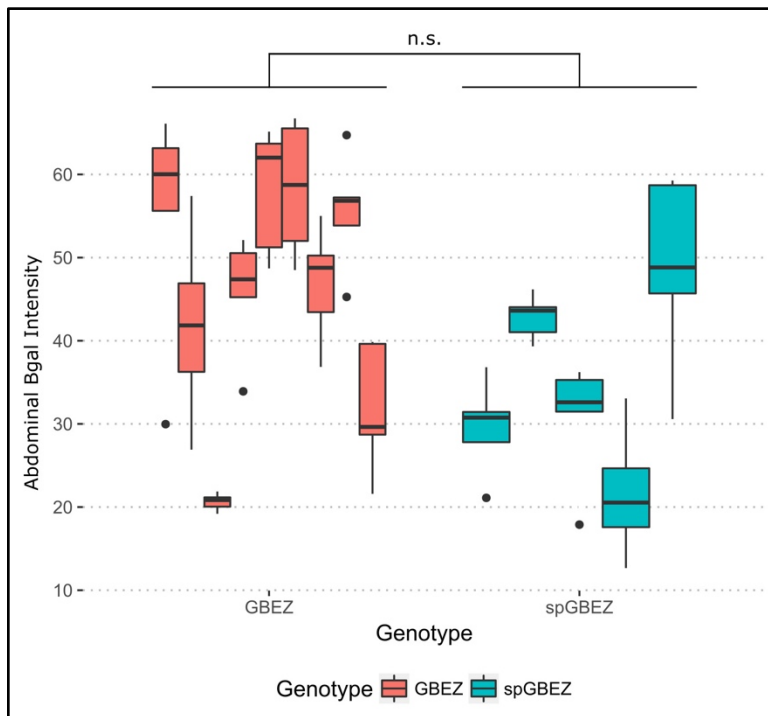


Figure S2. The *sp* sequence is transcriptionally inert. Quantification of β -gal immunostain intensity among abdominal Slp2+ cells in *G-LacZ* vs *spG-LacZ* reporter embryos.

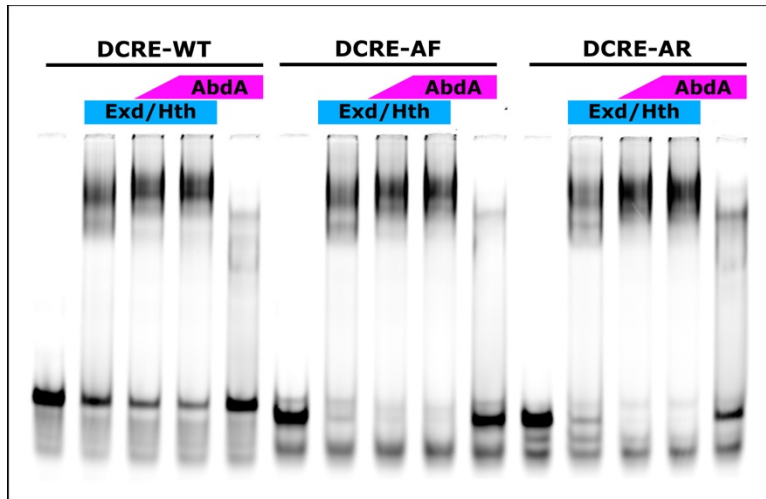


Figure S3. Comparative DNA binding analysis of Exd/Hth/Abd-A on wildtype, AR, and AF variants of *DCRE*. EMSA analysis of Exd/Hth/Abd-A on fluorescent probes of *DCRE* variants (wildtype, AR, and AF, see Figure 3B). Amounts of proteins added were as follows: 59ngs of Exd/Hth; 63ngs and 190ngs of Abd-A.

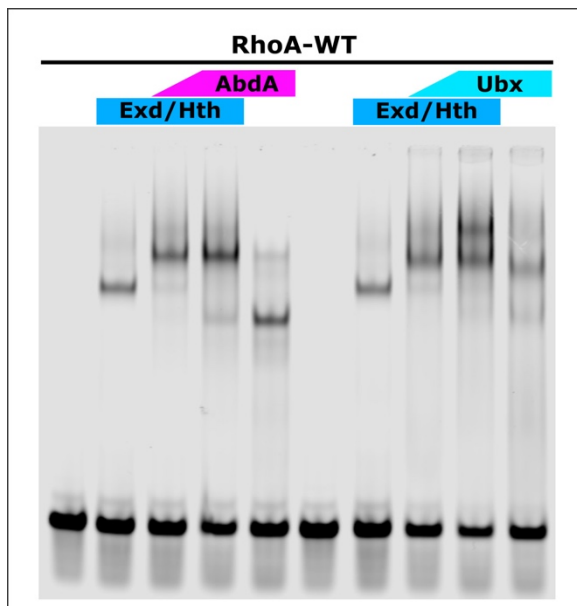


Figure S4. Comparative DNA binding analysis of Exd/Hth/Abd-A and Exd/Hth/Ubx on *RhoA*. EMSA analysis of Exd/Hth/Abd-A versus Exd/Hth/Ubx binding to fluorescent *RhoA* probe.

Amounts of proteins added were as follows: 59ngs of Exd/Hth; 63ngs and 190ngs of Abd-A; 80ngs and 240ngs of Ubx.

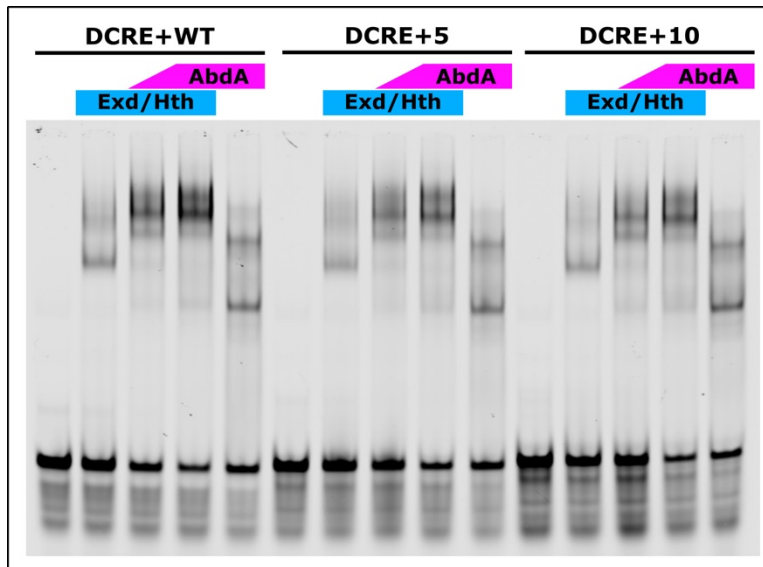


Figure S5. Comparative DNA binding analysis of Exd/Hth/Abd-A on wildtype, +5, and +10 variants of *DCRE*. EMSA analysis of Exd/Hth/Abd-A on fluorescent probes of *DCRE* variants (wildtype, +5, and +10, see Figure 4A). Amounts of proteins added were as follows: 59ngs of Exd/Hth; 63ngs and 190ngs of Abd-A.

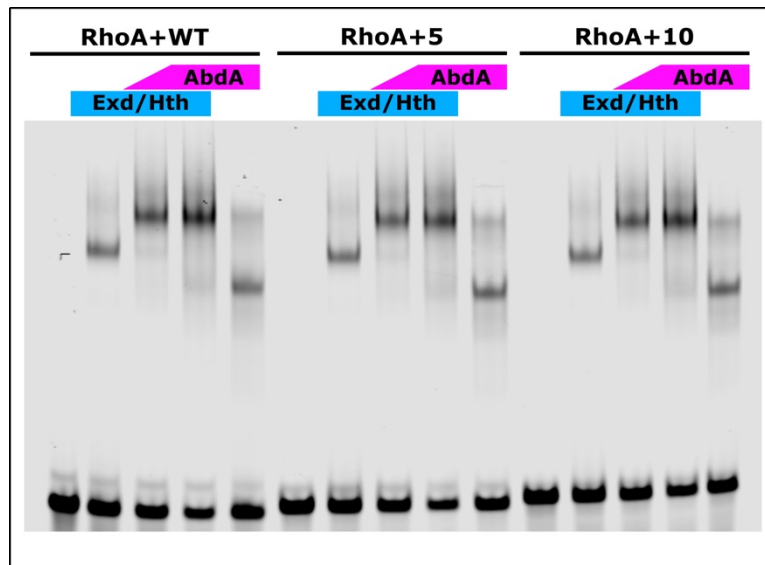


Figure S6. Comparative DNA binding analysis of Exd/Hth/Abd-A on wildtype, +5, and +10 variants of *RhoA*. EMSA analysis of Exd/Hth/Abd-A on fluorescent probes of *RhoA* variants (wildtype, +5, and +10, see Figure 5E). Amounts of proteins added were as follows: 59ngs of Exd/Hth; 63ngs and 190ngs of Abd-A.

